**Spencer Seale** | 208-949-5095 | spencerseale17@gmail.com | LinkedIn | GitHub

# Education

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|---|---|
| M.S. Bioinformatics | University of Oregon (2020) |
| B.S. Biology (Chemistry minor) | Seattle University (2016) |

# Experience

## TileDB

*Cambridge, MA*

**Sr. Bioinformatics Solutions Architect** Jan. 2025 – Present

**Bioinformatics Solutions Architect** Mar. 2024 – Dec. 2024

- Led technical engagements as a forward-deployed engineer for enterprise customers ($1M contracts), delivering hands-on engineering and consulting that contributed to successful renewals and contract expansions.
- Developed and maintained Python APIs used by thousands of open source and paying users, enabling programmatic access to TileDB.
- Utilized AI frameworks including MCP and RAG to improve LLM integration with TileDB, boosting agentic AI performance across the platform.
- Designed and implemented cloud-based (AWS, Argo, Nextflow) bioinformatics workflows (single-cell, population genomics, imaging, ML) capable of processing and querying terabyte-sized datasets, accelerating customer analyses.
- Mentored junior colleagues, improving team competency and productivity.

## Adaptive Biotechnologies

*Seattle, WA*

**Software Engineer III** Apr. 2023 – Mar. 2024

**Computational Biologist I** Nov. 2021 – Mar. 2023

**Computational Biology Associate II** Dec. 2020 – Nov. 2021

**Computational Biology Intern** Mar. 2020 – Dec. 2020

- Designed, developed, and deployed a multi-service bioinformatics pipeline (Python, R, Argo Workflows, Kubernetes, Azure, GitLab CI) supporting a novel product into production.
- Built an internal bioinformatics platform (Django, Docker, Azure) used by more than 50 scientists and engineers, streamlining tool access and automating 80% of routine analyses.
- Led the computational biology tool development group, releasing more than 10 software packages (built on CUDA, Docker, Kubernetes, Python, R) adopted company-wide by technical and non-technical users.
- Automated secondary analysis workflows using CronJobs and Azure Kubernetes Service, eliminating manual intervention by 90% and improving turnaround time.
- Orchestrated transition to cloud storage and computing, implementing Kubernetes automation, Azure Blob archival, and App Service hosting.

- Built and maintained a self-documenting CLI for storage and analysis pipelines, enabling “one-liner” data retrieval and processing.
- Mentored and managed comp bio developers via code reviews.
- Presented data-driven solutions to senior leadership, influencing adoption of new technologies and workflows across the department.
- Developed an R library of statistical tools adopted by a 40-member department, standardizing data analysis.
- Analyzed immune repertoire sequencing data for pharma and academic clients using statistical and analyses and presented work back to clients
- Investigated T-cell repertoire overlap in unrelated individuals, leading to publication.

### University of Oregon — *Eugene, OR*

**Graduate Teaching Fellow, Barkan Lab** — Sep. 2019 – Dec. 2019

- Delivered 10 lectures and labs on bioinformatics and genomics.
- Oversaw genomics-focused bioinformatics projects for student researchers.

### Fred Hutchinson Cancer Research Center — *Seattle, WA*

**Research Technician II, Geraghty Lab** — Oct. 2017 – June 2019

- Optimized a high-throughput library preparation assay for HLA typing, increasing assay throughput by 50% and transition to in-house consumables.

### Covance Genomics Laboratory — *Redmond, WA*

**Genomic Technologist** — July 2016 – Sep. 2017

- Performed over a thousand next-generation sequencing experiments, including library prep and sequencer operation, ensuring 99% data quality in a high-throughput lab.

## Technical Skills

**Languages**: Python, R, SQL, HTML/CSS

**Developer Tools & Frameworks**: Azure, AWS, Django, TileDB, CUDA, Streamlit, Shiny, Quarto, Anaconda, Pulumi, Nextflow, Argo Workflows, Helm, Git, Docker, GitLab CI, GitHub Actions, GitLab Pages, Bamboo CI, Jira, Linear, Kubernetes, VS Code, Postman, CronJob

**Favorite Python Libraries:** Poetry, Pandas, PyArrow, Pydantic, Attrs, NumPy, LangChain, PyTorch, Matplotlib, Black, Ruff, MyPy, Pre-commit, Pytest, TileDB-SOMA, Scanpy, CuPy, RAPIDS, Click, Sphinx, Quarto

**Concepts**: OOP, CI/CD, static typing, unit and acceptance testing, test mocking, cloud native storage/computing, on-disk database, cloud CLIs/SDKs, concurrent computing, event-driven automation, resource allocation, code portability, maintainability, readability, documentation

## Professional Highlights

**Publications:**

Johnson, S. A., **Seale, S. L.**, Gittelman, R. M., Rytlewski, J. A., Robins, H. S., & Fields, P. A. (2021). Impact of HLA type, age and chronic viral infection on peripheral T-cell receptor sharing between unrelated individuals. *PloS one*, *16*(8), e0249484. https://doi.org/10.1371/journal.pone.0249484

**Presentations:**

*Training Models on Atlas-scale Single-Cell Datasets* [GitHub]

**Awards:**

*The Helping Hand Award*, Adaptive Biotechnologies, 2022

- Recognized for cross-functional collaboration and spearheading a project that delivered a new software toolkit to computational biology department

*The Innovative Thinker Award*, Adaptive Biotechnologies, 2021

- Recognized for independently developing and deploying a software package that became a core part of team workflows, enabling fast, seamless querying of main software platforms.